Run on:

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310
406
410
RESULT
                                              June 1, 2003, 20:03:50 ; Search time 2844 Seconds (without alignments) 12710.382 Million cell updates/sec
                                                                           US-09-625-573-1
2232
1 GGATTGAACAAGACGCATT......TATAACTATGTTGATAAAAG 2232
                                                                                                                                                  32308132
         GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                      16154066 seqs, 8097743376 residues
                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                   OM nucleic - nucleic search, using sw model
                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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gb_htc:*
gb_est3:*
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gb_estl:*
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                                                                            Title:
Perfect.score:
Sequence:
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B6940587 ax06606.y
BB386118 BB386118
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R25491 yq44b06.r1
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BH281895 CH230-191
BR130511 601818643
AX417081 1M0192A12
AW960725 EST372796
BB630138 BB630138
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AA034154 H58597 H58245 H58245 H58245 A31312331 B642155 A31312331 B673536 AA671573 AA671573 AA671573 AA671573 AA671573 AA671573 AA671570 BB386318 RES909618 R

AI312331 ta78e11.x BG315432 PO2.0.308 BEP175316 MYE4866 M BI764263 60345953 AA671573 v104901.r BE656336 UI-M-BH0-AA673030 v280404.r AA673030 v280404.r AA673130 v10-M-BH0-BG292833 602389845 AA318949 EST21122

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ALIGNMENTS

AU127682 AU127682 AU140261 AU140261 BG104799 602311755 AZ713219 RPCI-24-1

		zi42a04.sl Soares_fetal_l	AA694175	AA694175.1 GI:2695113	EST.	human.		Eukaryota, Metazoa, Chordata, Craniata, Vertebiata, bucereoscomit,	1 (bases 1 to 45/)		Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, Martin	J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Therstuy, B.,	White, Y., Wylie, T., Waterston, R. and Wilson, K.	WashU-NCI human EST Project			Washington University School of Medicine	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Tel: 314 286 1800	Fax: 314 286 1810	Email: est@watson.wustl.edu	This clone is available royalty-free through LLNL; contact the	IMAGE Consortium (info@image.llnl.gov) for further infommation.	Seq primer: -40m13 fwd. ET from Amersham	High quality sequence stop: 455.	
110001	AA694175/c	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS				TITLE	JOURNAL	COMMENT										

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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Query Match Length DB

Result

AA694175 z142a04.s BQ027284 UI-H-COO-AV715904 AV715904 AA807940 nu90f10.s AA034153 z106f10.r H58584 yr06f06.r1

AA694175 BQ027284 AV715904 AA807940 AA034153 H58584

114 10 14

17.7 16.4 16.1 15.8 12.2

396 367 359 352 272 243

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Description

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Query Match
Best Local Similarity
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                                                                                                                                            source
            JOURNAL
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1 (bases 1 to 407)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                  1832 TTGGCTTCTAATCAAAGCTTTTAAACCCTATTGGTAAAGAATGGAAGGTGGAAGCTCC 1891
                                                                                                                                                                                                                                                                                                                                             1892 CTGAAGTAAGCAAAGACTTTCCTCTTAGTCGAGCCAAGTTAAGAATGTTCTTATGTTGCC 1951
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UI-H-COO-aqo-h-07-0-UI.sl NCI_CGAP_Sub9 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2192 ATTIGGAAAATAAATCAATGCTATAACTATGTTGAT 2227
                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                               _xref="GDB:1333191"
                                             /db_xref="taxon:9606"
                                                       /clone="IMAGE:433422"
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ027284.1 GI:19762563
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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            source
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/dev_astee="maxed"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73 Pac (Pharmacia) with a modified
/note="Vector: pT73 Pac (Pharmacia) with a modified
/note="Vector: pT73 Pac (Pharmacia) with a modified
polylinker; Site=1: EcoR I; Site=2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain ligodenece Contract of Non Synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded CDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
information, contact: Bento Soares, bento-soares@ulowa.edu
                                                  Email: cgapbs remail.nl.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 367; DB 14; Length 407; 100.0%; Pred. No. 5.2e-185; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_LIB=U1-H-CO0
TAG_LIBSUB=Cervical Adenosquamous Carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="INAGE:3104867"
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                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Unpublished (1997)
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LOCUS

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Viote="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified Polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
a 87 c 73 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contract: No. 12. (1) Contract: Robert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLone distribution: NGLCGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.blo.lln.gov/bbrp/image/image/image.html
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 385.
                                                                                                                  AA807940 398 bp mRNA linear EST 12-FEB-1998
nu90f10.sl NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1217995 3',
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 398)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NXIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1892 CTGAAGTAAGCAAAGACTTTCCTCTTAGTCGAGCCAAGTTAAGAATGTTCTTATGTTGCC 1951
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414 CTCCATCGCTGTCATCTCAGCTGGATCTCCATTCTCTCAGGCTTGCTGCC 463
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Pred. No. 5.8
Matches 352; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                     mRNA sequence.
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                                                                                      RESULT 4
AA807940/c
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                                                                                                                                                                                                            ACCESSION
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                                                                                                                                                           AV715904 DCB Homo sapiens cDNA clone DCBAMF09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                  Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Crarrhini; Hominidae; Homo

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ku,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,

Song,H., Gu,Y., Yang,X., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,

Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Cheng,Z. and Han,Z.

Gong, And Hon,Z.

Homo sapiens cDNA DCB clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chinese National Human Genome Center at Shanghal 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghal 201203, P. R. China 181: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
81 c 109 g 146 t
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Best Local Similarity 99.8%; Pred. No. 1e-180;
Matches 409; Conservative 0; Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
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                                                                                                                                                                                                                                                AV715904.1 GI:10797421
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                                                     24 ATGTTGA 18
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                                 BASE COUNT
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1 (bases 1 to 563)
Hillier,L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dudque,T., Favello,A., Gish,W., Hawkins
'M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
'B., Morris,M., Parsons,J., Pranqe,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                           ziO6f10_r1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:430027 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidee, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 432 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 305.
1437 CTATCATGTCAAACGTGAAAATGCTGTATTAGTCACAGAGATAATTCTAGCTTTGAGCTT 1496
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                                                2132 GAATGCATAAAATGTTAAGTTGATGGTGAAGTGTAAATACTGTTTTAA 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:430027"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                  Length 563;
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100.0%; Pred. No. 4.9e-134;
.ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:1329796"
                                                                                                                                                                                                                                           AA034153.1 GI:1505981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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Matches 272; Conservative
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/db_xref="taxon:9660"
/db_xref="taxon:9660"
/clone="InAGE:204515"
/clone="InAGE:204515"
/dev_stage="20 week-post conception fetus"
/dev_stage="20 week-post conception"
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Leh.M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H58584
Yr06f06.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone IMAGE:204515 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1497 AAGAATITTGAGCAGGTGGTATGTTTGGGAGACTGCTGAGTCAACCCAATAGTTGTTGAT 1556
                                                                                                                                           1557 IGGCAGGAGTIGGAAGIGIGIGATCIGIGGGCACATTAGCCIATGIGCAIGCAGCAICTA 1616
                                                                                                                                                                                                                                                                                       Email: est@watch.edu
Insert Size: 1007
High quality sequence stops: 300
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: M13RP1
                                                                                                                                                                                  constructed by Bento Soares and M.Fatima Bonaldo." 66 c 94 g 140 t
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                           1677 CAITCICICAGGCTIGCIGCCAAAAGCCITIT 1708
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Location/Qualifiers
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H58584
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10.9%; Score 243; DB 14; Length 410;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I: (bases 1 to 422)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultmanson, A., Wohldmann, P. and Wilson, R.
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Marck EST Project
I Onpublished (1995)
Contact: Wilson RK
Washington Oniversity School of Medicine
Mashington Oniversity School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pr773D (Pharmacla)
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H58597 1. Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1025 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                      1995 IAGAACCAGGCAACTIGGGAACTAGACTCCCAAGCIGGACTAIGGCICIACITICAGGCC 2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2115 ATTTGTATGATCCTAATGCATAAAATGTTAAGTTGATGGTGATGAAATGTAAATAC 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2055 ACAIGGCTAAAGAAGGTTTCAGAAAGAAGTGGGGACAGAGCAGAACTTTCACCTTCATAT 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                         238 TAGAACCAGGCAACTTGGGAACTAGACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares fetal liver spleen lNFLS"
/sex="male"
                                                                                                                                                                                                                                                                     10.7%; Score 238; DB 9; Length 289; 100.0%; Pred. No. 7.6e-116; tive 0; Mismatches 0; Indels
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Matches 238; Conservative
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H58597
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 289)
1 (bases I to 280)
1 (bases I to 280)
2 (bases I to 280)
2 (bases I to 280)
2 (bases I to 280)
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen livers library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 09-MAY-1997
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (life@image.llnl.gov) for further information.
Insert Length: 432 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 202.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 bp mRNA linear EST 09-MAY-1 close IMAGE:430027 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            1487 CITTGAGCTTAAGAATTTTGAGCAGGTGGTATGTTTGGGAGACTGCTGAGTCAACCCAAT 1546
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/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                     Indels
                                         Pred. No. 1.7e-118;
                                                                     0; Mismatches
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/db_xref="GDB:1329796"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA034154.1 GI:1505982
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                                             99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                            293; Conservative
                                         Best Local Similarity
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EMARGADIS Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Muchaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R., Williamson,A., Wohldmann,P. and Wilson,R.

The Washur Merck EST Project

Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1800
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; Ist strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATAAAAAAGATTTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to Eco RI adaptors and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yr06h06.s1 Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
IMAGE:204539 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                             1367 TAAATAGTAAAAATAAAATTAAAGCTGAAAACTGCAACTTGTAAATGTGGTAAAGAGTTA 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Size: 1025
High quality sequence stops: 344
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1025 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGTIGITGATIGGCAGGAGTIGGAAGTGTGTGATCTGTGGGCACATTAGCCTATGTGCAT 240
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Pred. No. 9.5e-115;
0; Mismatches 1; Indels (
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/db_xref="GDB:3773670"
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Location/Qualifiers
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                                                                                                                                                                                                                                               10.6%;
99.7%;
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H58254/c
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EST 05-0CT-1995
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IMAGE:204515 3', mRNA sequence.
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Hillar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Leh.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Marck EST Project
Unpublished (1995)
Contact: Wilson RK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        2000 CCAGGCAACTIGGGAACTAGACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCCACATG 2059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 1007
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1007 Std Error: 0.00
Seq primer: Promega - 21ml3
High quality sequence stop: 335.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                   /clone_lib="Soares fetal liver spleen INFLS"
                                                                                                                                                                                                                                                                                                                                  10.4%; Score 232; DB 14; Length 467; 100.0%; Pred. No. 1.3e-112; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 bp
/db_xref="taxon:9606"
/clone="IMAGE:204539"
                                                      /sex="male"
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Matches 232; Conservative
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CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Www.bio.llnl.gov/bbrp/jmage/lmage.html
Insert Length: 266 Std Error: 0.00
Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI312331 176 bp mRNA linear EST 18-MAR-1999
ta78e11.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050220 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 176)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                       /note="Vector: pBAde3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
103 c 113 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 TICGGCCTGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACGCAGGTGACAGAG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.7%; Score 128; DB 17; Length 469; Local Similarity 100.0%; Pred. No. 8e-57; es 128; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                               8e-57;
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/tissue_type="stem cell 34+/38+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7508309"
/db_xref="taxon:9606"
                                                                                                                                                                                                                      /sex="Male"
/cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2050220"
                                                                                                                                                                           /clone="RPCI-11-22K6"
/clone_lib="RPCI-11"
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                                                                     Location/Qualifiers
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AI312331
AI312331.1 GI:4017936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 128; Conservative
                                                                                            1. .469
                               Seq primer: T7
Class: BAC ends.
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1 (bases 1 to 469)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCIII-22K6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22K6, DNA
                                                                                                                                                                                                                                                                                         double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTyT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences for Sequence-Ready Map Building (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match B.0%; Score 179; DB 14; Length 461; Local Similarity 99.6%; Pred. No. 3.6e-84; es 229; Conservative 0; Mismatches 1; Indels (
                                                                                            /clone="IMAGE:204515"
/clone_lib="Soares fetal liver spleen 1NFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Far: 301 838 0200
Fax: 301 838 0208
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                                             /organism="Homo sapiens"
/db_xref="GDB:3773646"
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Other_GSSs: RPCI11-22K6.TP
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases I to 207)
Andersson, T., Borang, S., Larsson, M., Thelin, A., Ekstrand-Hammarsrom, B., Wirta, V., Wenborg, A., Lundeberg, J. and Odeberg, J. virtual chipathification of candidate genes in atherosclerosis - Virtual chipanalysis in RDA based transcript profiling of monocyte/macrophage
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bone marrow, stem cells 34+/38+, cDNA made by oligo-dr
priming. Directionally cloned. Size-selected on agarose
qel, average insert size 400 bp. Primary library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2011-152 2012 MRNA linear EST 28-FEB-2002 PD2.0.308 Human THP1 cell line library Homo sapiens cDNA, mRNA
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/db_xref="taxon:g606"
/clone_lib="Human THP1 cell line library"
/cell_line="THP1" site_1: BamH1; Site_2: BamH1;
/note="Vector: pRIT28; Site_1: BamH1; Site_2: BamH1;
Shotgun cloning of RDA difference products. Macrophage and foamcell libraries were submitted to successive rounds of subtractive hybridisations generating populations of gene fragments that are differentially expressed in macrophage
to coam cell formation."

4 5 5 4 3 others
                                                                                                                                                                                                                      1290 GGGTTGGAAAACAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTTGAATACAGGCAT 1349
                                                                                                                                                                                                                                                                                                  1350 AGAGTICAGACTITITITAAATAGTAAAATAAATTAAAGCTGAAAACTGCAACTTGTA 1409
                                                                                                                                                                                                                                                                                                                       0; Gaps
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Tel: +46 8 790 71 29
Fax: +46 8 245452
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Mismatches 0; Indels
                                          gel, average insert size 400 bp.
non-amplified. " 44 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tove@biochem.kth.se
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Best Local Similarity 100.(
Matches 108; Conservative
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//wew_actge="Mucticipie mystoma" / note="WetCor: Lambda Zap Express; Site_1: EcoRI; Site_2: Motor: Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the CDNAs from XhoI digestion in subsequent cloning step, the nucleotide malogue 5-methyl-dCTP was added to the nucleotide malogue 5-methyl-dCTP was added to monitor the quantity and quality of first strand synthesis. After second strand synthesis and blunting of CDNA termin, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then slate into EcoRI and XhoI digested Lambda 22D Express vector. The ligation product was packaged using Giapack Theathy and primary titre of approx. 1x106 clones from the primary library were randomly selected for single pass sequencing."
                                                                                                                                                                              EST 23-MAR-2001
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1 (bases 1 to 121)
Claudio, J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E., Franciso-Pabalan, O., Liew, C.C. and Stewart, A.K.
The transcriptional phenotype of myeloma cells
Contact: A. Keith. Stewart, M.D.
Onclogy Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University Health Network
610 University Ave., 5-126, Toronto, Ontario, MSG 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
Email: K.stewart@utconto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                   MYE4866 Myeloma (MYE) cDNA library Homo sapiens cDNA, mRNA
3.0%; Score 68; DB 12; Length 121;
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: 5'-GCCAAGGTCGAAATTAACCCICACIAATAGGGCG-3'
BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seg primer: 5'-GAAATTAACCCTCACTAAAGG-3'.
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/sex="male"
                                                                                                                                                                            mRNA
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/dev_stage="multiple myeloma"
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/db_xref="taxon:9606"
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/note="Organ: pooled colon, kidney, stomach; Vector: pcMv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male end 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned EcoRV site is destroyed upon cloning). Library is normalized and insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
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603045953F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186388 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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